

# Package 'PWMErich.Dmelanogaster.background'

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**License** GPL-3

**Title** D. melanogaster background for PWMErich

**Type** Package

**LazyLoad** yes

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**Description** PWMErich pre-compiled background objects for Drosophila melanogaster and MotifDb D. melanogaster motifs.

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**biocViews** Drosophila\_melanogaster\_Data

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**Depends** R (>= 2.10), methods, PWMErich

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 PWMErich.Dmelanogaster.background-package

*PWMErich.Dmelanogaster.background package overview*


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## Description

This package provides a set of pre-compiled genomic background files for the PWMErich package and *D. melanogaster*. The backgrounds were pre-compiled using unique promoters of *Drosophila melanogaster*.

- `MotifDb.Dmel.PFM` - a list of 740 position frequency matrices (PFMs) from `MotifDb`
- `MotifDb.Dmel` - the corresponding PWMs generated by using the background frequencies of A,C,G,T in a set of 10031 2kb promoters in *D. Melanogaster*.
- `PWMLogn.dm3.MotifDb.Dmel` - pre-compiled threshold-free lognormal background for JASPAR insects PWMs. The lognormal distribution is fitted to 1kb fragments of 10031 2kb *Drosophila Melanogaster* (dm3) promoters. For each gene one promoter is taken (from the first transcript).
- `PWMCutoff4.dm3.MotifDb.Dmel`, `PWMCutoff5.dm3.MotifDb.Dmel` - pre-compiled Z-score background with cutoff of 4 and 5 (base e) for JASPAR insects PWMs. The number of hits above the score cutoff is counted in 10031 2kb *Drosophila Melanogaster* (dm3) promoters. For each gene one promoter is taken (from the first transcript).
- `PWMPvalueCutoff1e2.dm3.MotifDb.Dmel`, `PPWMPvalueCutoff1e3.dm3.MotifDb.Dmel`, `PPWMPvalueCutoff1e4.dm3.MotifDb.Dmel` - pre-compiled Z-score background with P-value cutoff of 0.01, 0.001, and 0.0001 for JASPAR insects PWMs. The number of hits with smaller P-value than cutoff is counted in 10031 2kb *Drosophila Melanogaster* (dm3) promoters. For each gene one promoter is taken (from the first transcript).

## Usage

```
data(MotifDb.Dmel.PFM)
data(MotifDb.Dmel)
data(PWMLogn.dm3.MotifDb.Dmel)
data(PWMCutoff4.dm3.MotifDb.Dmel)
data(PWMCutoff5.dm3.MotifDb.Dmel)
data(PWMPvalueCutoff1e2.dm3.MotifDb.Dmel)
data(PWMPvalueCutoff1e3.dm3.MotifDb.Dmel)
data(PWMPvalueCutoff1e4.dm3.MotifDb.Dmel)
```

## Details

All of these objects were created with the appropriate functions available in the PWMErich package (see Section 'See also'). We recommend using these functions to generate backgrounds for a custom set of background sequences and/or DNA motifs.

This package also contains the 2kb upstream sequences for *Drosophila* genes (`dm3.upstream2000`) which were removed from the `BSgenome.Dmelanogaster.UCSC.dm3` package starting from Bioconductor version 3.0.

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**See Also**

[makeBackground](#), [makePWMLognBackground](#), [makePWMCutoffBackground](#), [makePWMEmpiricalBackground](#).

**Examples**

```
data(PWMLogn.dm3.MotifDb.Dmel)

res = motifEnrichment(DNAString("TGCATCAAGTGTAGTGCGATGAATGC"), PWMLogn.dm3.MotifDb.Dmel)

head(motifRankingForGroup(res))
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